

(1) GENERAL INFORMATION:

(1) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie

(ii) TITLE OF INVENTION: Stimulation of angiogenesis via enhanced endothelial expression of syndecan-4 core proteins

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David Prashker, Esq.
(B) STREET: P.O. Box 5387
(C) CITY: Magnolia
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 01930

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
(B) COMPUTER: Dell PC
(C) OPERATING SYSTEM: MS DOS
(D) SOFTWARE: Microsoft Word version 97

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/145,916
(B) FILING DATE: September 2, 1998
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: David Prashker, Esq.
(B) REGISTRATION NUMBER: 29,693
(C) REFERENCE/DOCKET NUMBER: BIS-039

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGCGCGCTCTG GCTTGGCTC TGCGCGCTGG CGCTGCCT GCAGCCTGCC 60
CTCCCGAAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGACGAC 120
TCAGACAAC TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAGCAGGG ATACCGAGGC CACCCCTCAC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGGAAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGGAG 360
AAGGGAGCCA CCACCAAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
ACAGCAGCCA GAGCCACAC GGCCAGGCA TCTGTCACGT CTCACTCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
AATCAGCTTC CTGCAAGGAGA GGGCTCTGGA AAACAAGACT TCACCTTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGGCCTTTG GACAGGAAGG AA 762

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
 GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
 GCTGCTCTCC AGATAACCCC GGAGCTCCAG CGCGCGGGAT CGCGCGCTCC CGCCGCTCTG 180
 CCCCTAAACT TCTGCCGTAG CTCCCTTCA AGCAGCGAA TTTATTCCCT AAAACCAGAA 240
 ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
 AGCTTCAGAG AGCAGCCTTC CGGGAGCACC AACTCCGTGT CGGGAGTGCAGA GAAACCAACA 360
 AGTGAGAGGG CGCCGCGTTC CGGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
 AGGAAGCGAG CGCCCCCGAG CCCCGAGGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
 GGTACTCTGC TCCGGATTCTG TGTGCCGGGG CTCGCCGAGC GCTGGGGCAGG AGGCTTCGTT 540
 TTGCCCTGGT TCGAACGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT CGGGCGCGC 600
 TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCGTGTGCG CGGAGTCCAG AGCAGAGCTG 660
 ACATCTGATA AAGACATGTA CCTTGACAAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
 CCTATTGATG AGCATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
 AGTCCAGAGC TGACAAACAC TCGACCACCTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
 AAAGTGGAAA CCACGACGCT GAATATACAG AACAGATAC CTGCTCAGAC AAAGTCACCT 900
 GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAT GGACCCAGCC 960
 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTAA ACGGACAGAA 1020

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly	Arg	Arg	Glu	Gly	Ala	Arg	Gly	Lys	Glu	Glu	Glu	Glu	Glu		
1								10					15		
Asp	Pro	Gly	Arg	Glu	Ala	Arg	Gly	Arg	Arg	Arg	Gly	Ala	Ala		
								20		25			30		
Glu	Pro	Val	Ala	Pro	Leu	Gly	Arg	Ala	Ala	Leu	Gln	Ile	Pro	Pro	Glu
								35		40			45		
Leu	Gln	Pro	Arg	Gly	Ser	Arg	Ala	Pro	Ala	Ala	Leu	Pro	Leu	Asn	Phe
								50		55			60		
Cys	Arg	Ser	Ser	Leu	Ser	Ser	Gln	Arg	Ile	Tyr	Ser	Leu	Lys	Pro	Glu
								65		70			75		80
Thr	Glu	Pro	Arg	His	Gly	Lys	Gly	Val	Arg	Gly	Gly	Ala	Lys	Pro	Gln
								85		90			95		
Gln	Ser	Lys	Lys	Ser	Phe	Arg	Glu	Gln	Pro	Ser	Arg	Ser	Thr	Asn	Ser
								100		105			110		
Val	Ser	Gly	Val	Gln	Lys	Pro	Thr	Ser	Glu	Arg	Ala	Pro	Arg	Ser	Arg
								115		120			125		
Gly	Ala	Ala	Ala	Gly	Gly	Ser	Arg	Arg	Arg	Arg	Arg	Lys	Arg	Ala	
								130		135			140		
Pro	Pro	Ser	Pro	Glu	Pro	Glu	Ser	Pro	Ser	Leu	Ser	Arg	Asn	Arg	Cys
								145		150			155		160
Gly	Thr	Leu	Leu	Arg	Ile	Arg	Val	Arg	Gly	Leu	Ala	Glu	Arg	Trp	Ala
								165		170			175		
Gly	Gly	Phe	Val	Leu	Pro	Trp	Leu	Gln	Ala	Ala	Ala	Gly	Ser	Ser	Arg
								180		185			190		
Ser	Leu	Gly	Asn	Met	Arg	Arg	Ala	Trp	Ile	Leu	Leu	Thr	Leu	Gly	Leu
								195		200			205		
Val	Ala	Cys	Val	Ser	Ala	Glu	Ser	Arg	Ala	Glu	Leu	Thr	Ser	Asp	Lys
								210		215			220		

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Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
225 230 235 240
Pro Ile Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
245 250 255
Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
260 265 270
Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Leu Asn
275 280 285
Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
290 295 300
Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
305 310 315 320
Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
325 330 335
Lys Arg Thr Glu
340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCAGCGAG CTGGCGGCC 60
TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGA TGATGATCCC TTTGGGGACG 180
ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
TGGAGACAGC GGTCAAGCCTC ACCACGGACA CGTCCGTCCTC ACTGCCCACC ACGGTGGCCG 300
TGCTGCCTGT CACCTGGTG CAGCCCCATGG CAACACCCCT TGAGCTGTC CCCACAGAGG 360
ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAAG 420
TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
CCTCCACCAAC CACCAACCACG GCTGCTACCA CCACCAACAAC CACCAACCAC ATCAGCACCA 540
CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTC GCCCCCCCTT GTCACCAAGG 600
CAGCCACAC CCGGGCCACC ACCCTGGAGA CGCCACCCAC CTCCATCCCT GAAACCAAGTG 660
TCCITGACAGA GGTGACCAACA TCACGGCTTG TCCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
TGCCAAAACC AACGCACTTCC AGGACTGCAG AACCCACCGA AAAAACACT GCCTTGCCTT 780
CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGGCCAGGG GAGTTGACGA 840
CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
TCCAGGAGGA GGAGGAGACA ACTCGTCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
CACCACCAAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCAGCGCTG CTGCTGTTGC TCCCTGGAGG TTTCCCCGTC 60
GCCCCAGCG AGTCGATTGAG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180
GACTTTGAGC TGTCGGGTTG CCGAGATCTA GATGACACGG AGGAGCCCAAG GACCTTCCT 240
GAGGTGATTT CACCCCTGGT GCCACTAGAT ACCACATCC CCGAGAATGC CCAGCCTGGC 300

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ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCAATTCC CAAAAGGGTC 360
CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
GGCAGCAACA TTTTGAAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCGCA GATCTACGGG 120
GCTAAGGGCT TTAGCCTGAG CGACGTGCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
ATCTGCCCTT AGGGCTACAC CTGCTGCACC AGTGAAGATGG AGGAGAACCT GGCCAACCAC 240
AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
ACACTGCAGG ATGCTTTCTC CGGGGCCCTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
TTCCGGGACC TGTATGCTGA GCTGCCTCTC TACTACCGAG GGGCCAAACCT ACACCTTGAG 480
GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCCTGGCA AGCAGGCAGA GGCACCTGCGG 600
CCGTTGGGG ATGCCCTCTG AGAAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
CGATCCTTG TGCAGGGCCT GGGTGTGGCC AGTGAACGTAG TCCGAAAGGT GGCCCAAGGTT 720
CCTCTGGCCC CAGAATGTTC TCAGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATGCCGG 780
GGAGTCCCTG GTGCCCGGCC CTGTCCCAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
GCCAACCAAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
ACTGACAAGT TCTGGGGCCC GTGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAAGGACA CACTCACAGC TAAGGTCACTC 1020
CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
GAGGCCAAGG CCCAGCTCCG AGACATTCA GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTC 1260
AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCCT 1320
GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
AAGATCATGA CCAACCGTT ACGTGGGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
GCCAGTQATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCT TGACCCATGC CCTCCCCGGC 1560
TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1 5 10 15
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
20 25 30
Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
35 40 45
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
50 55 60
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His

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65	70	75	80
Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu			
85	90	95	
Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln			
100	105	110	
Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly			
115	120	125	
Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu			
130	135	140	
Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu			
145	150	155	160
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys			
165	170	175	
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu			
180	185	190	
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu			
195	200	205	
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val			
210	215	220	
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val			
225	230	235	240
Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys			
245	250	255	
Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys			
260	265	270	
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala			
275	280	285	
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe			
290	295	300	
Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser Val His Met Trp			
305	310	315	320
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr			
325	330	335	
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro His Gly			
340	345	350	
Ser Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Leu Gln Glu			
355	360	365	
Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala			
370	375	380	
Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu Pro Gly Thr Leu			
385	390	395	400
Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp			
405	410	415	
Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly			
420	425	430	
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys			
435	440	445	
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr			
450	455	460	
Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp			
465	470	475	480
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Cys Pro Asp			
485	490	495	
Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Arg Thr			
500	505	510	
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys			
515	520	525	

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Thr Ser Ala
530

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCCTAGGAG GTGTCATTGC TGGAGGCCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60
GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTC TCTTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1 5 10 15
Ile Phe Leu Ile Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCCCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GTCTTGGCAG CTCTGATTGT GGGCGCCGTA GTGGGCATCC TCTTCGCCGT TTTCTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60
GCTGCAGCCA GGCCCAGGTG GCGGTAAC TG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr
1 5 10 15
Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
20 25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCGCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCCTCT GGGCGAGTGG GGG

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGGAACCATG GCGCCTGTCT GCC

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCAG GTTTTATTAT CTTTTTATC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTCAC CAGGGC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTTCG

26

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys

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